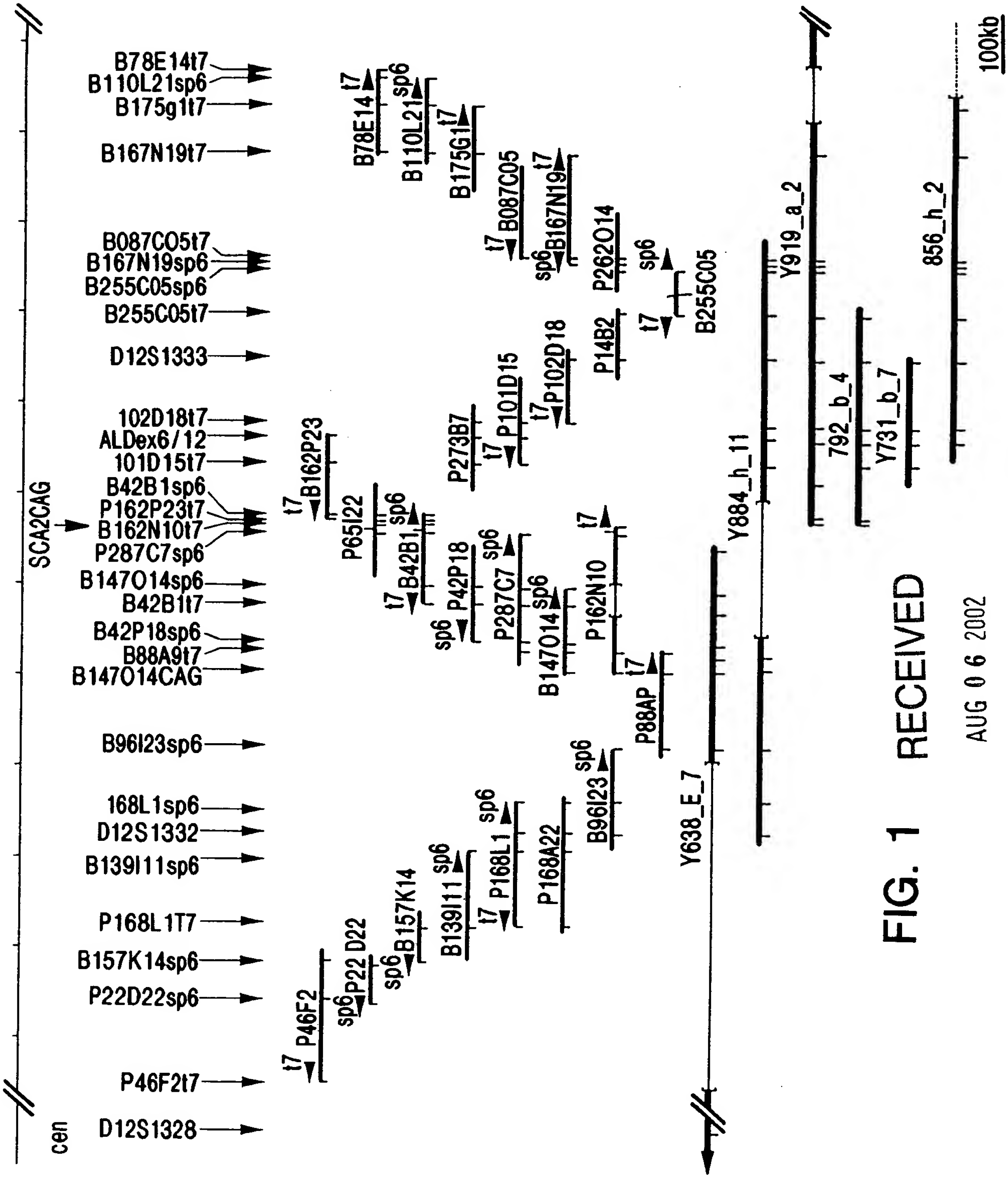
B78E14t7
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B167N19t7
B087C05t7
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B255C05sp6
B255C05t7
D12S1333
102D18t7
ALDex6/12
101D15t7
B42B1sp6
SCA2CAG
P162P23t7
B162N10t7
P287C7sp6
B147O14sp6
B42B1t7
B42P18sp6
B88A9t7
B147O14CAG
B96I23sp6
168L1sp6
D12S1332
B139I11sp6
P168L1T7
B157K14sp6
P22D22sp6
P46F2t7
cen
D12S1328
B78E14
B110L21
B175G1
B087C05
B167N19
P262O14
B255C05
P14B2
P102D18
P101D15
P273B7
B162P23
P65I22
B42B1
P42P18
P287C7
B147O14
P162N10
P88AP
B96I23
P168A22
P168L1
B139I11
B157K14
P22D22
P46F2
t7
sp6
Y919_a_2
856_h_2
792_b_4
Y731_b_7
Y884_h_11
Y638_E_7
100kb

FIG. 1

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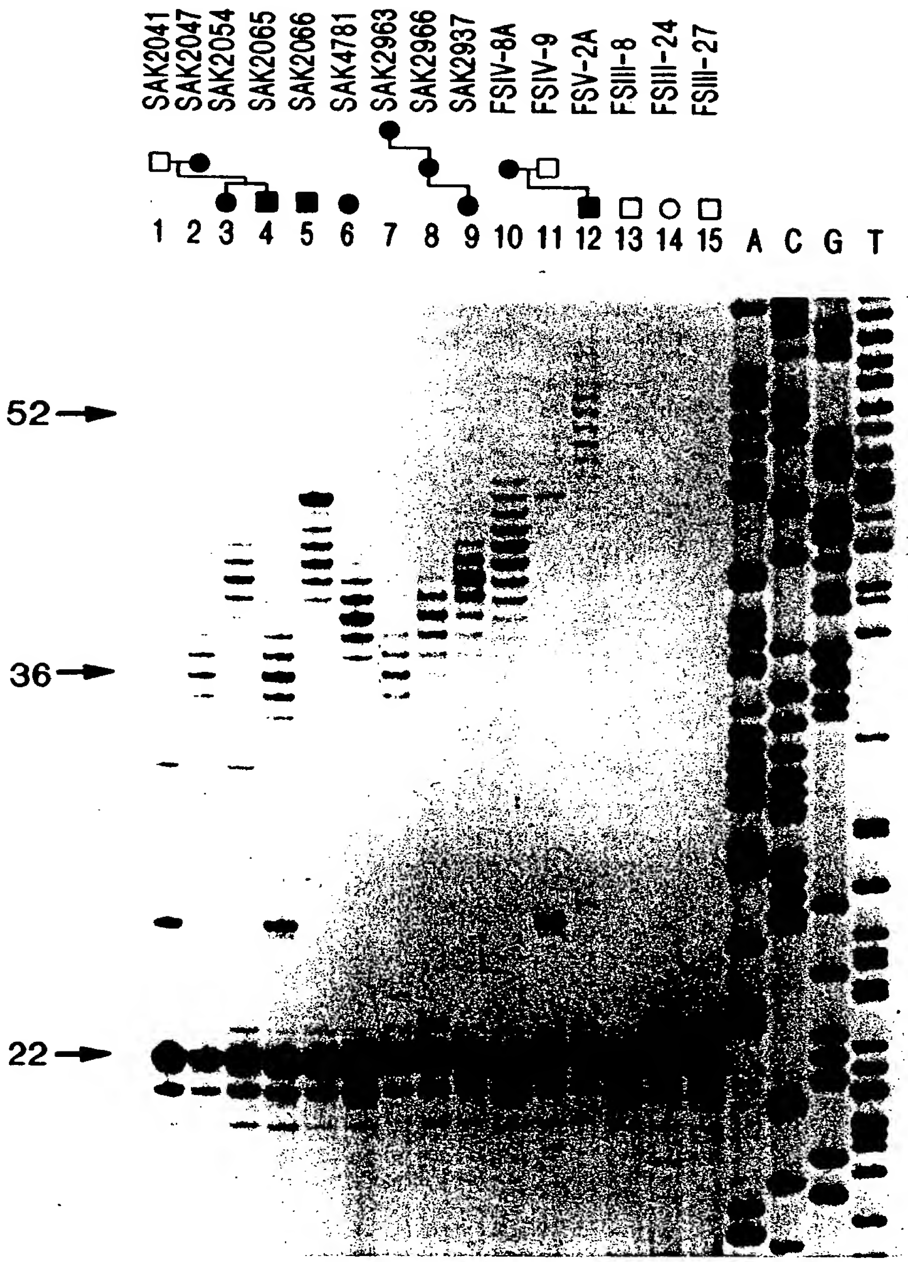
```
1    TTGGTAGCAACGGAAACGGCGGCGGCGCGTTTCGGCCCGGCTCCCGGCGGCTCCTTGGTC

61   TCGGCGGGCCTCCCCGCCCCTTCGTCGTCGTCCTTCTCCCCCTCGCCAGCCCGGGCGCCC

121  CTCCGGCCGCGCCAACCCGCGCCTCCCCGCTCGGCGCCCGTGCGTCCCCGCCGCGTTCCG

181  GCGTCTCCTTGGCGCGCCCGGCTCCCGGCTGTCCCCGCCCGGCGTGCGAGCCGGTGTATG
          SCA2-A
241  GGCCCCTCACCATGTCGCTGAAGCCCCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGC
                                                            SCA2-B
301  AGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCCGCCGCCCGCGGCTGCCAATGTCCGCA

361  AGCCCGGCGGCAGCGGCCTTCTAGCGTCGCCCGCCGCCGCGCCTTCGCCGTCCTCGTCCT

421  CGGTCTCCTCGTCCTCGGCCACGGCTCCCTCCTCGGTGGTCGCGGCGACCTCCGGCGGCG

481  GGAGGCCCGGCCTGGGCAG GTGGGTGTCGGCACCCC
```

FIG. 2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SAK2047
SAK2054
SAK2065
SAK2066
SAK4781
SAK2963
SAK2966
SAK2937
FSIV-8A
FSIV-9
FSV-2A
FSIII-8
FSIII-24
FSIII-27
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 A C G T
52
36
22

FIG. 3

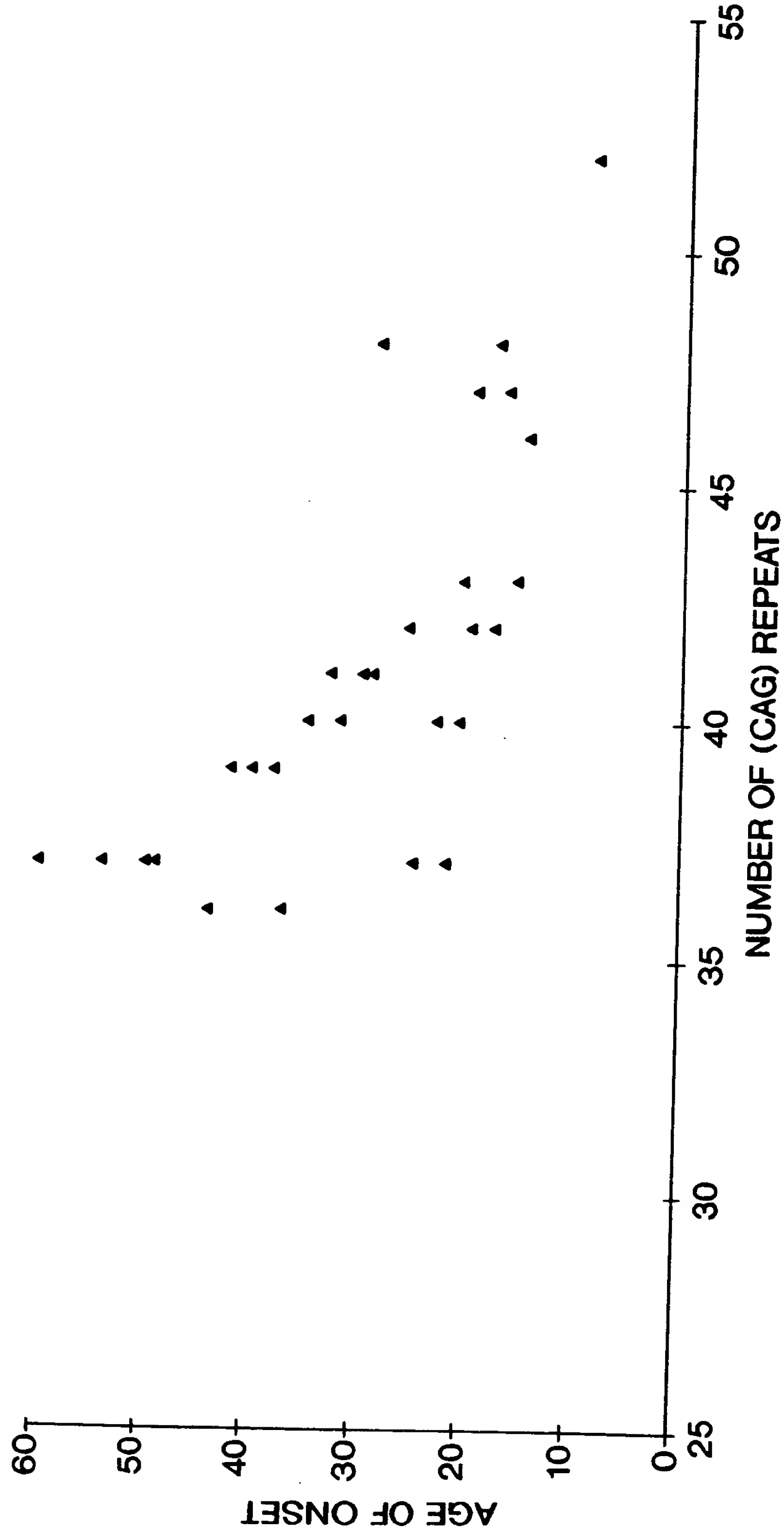

AGE OF ONSET
0
10
20
30
40
50
60
NUMBER OF (CAG) REPEATS
25
30
35
40
45
50
55

FIG. 4

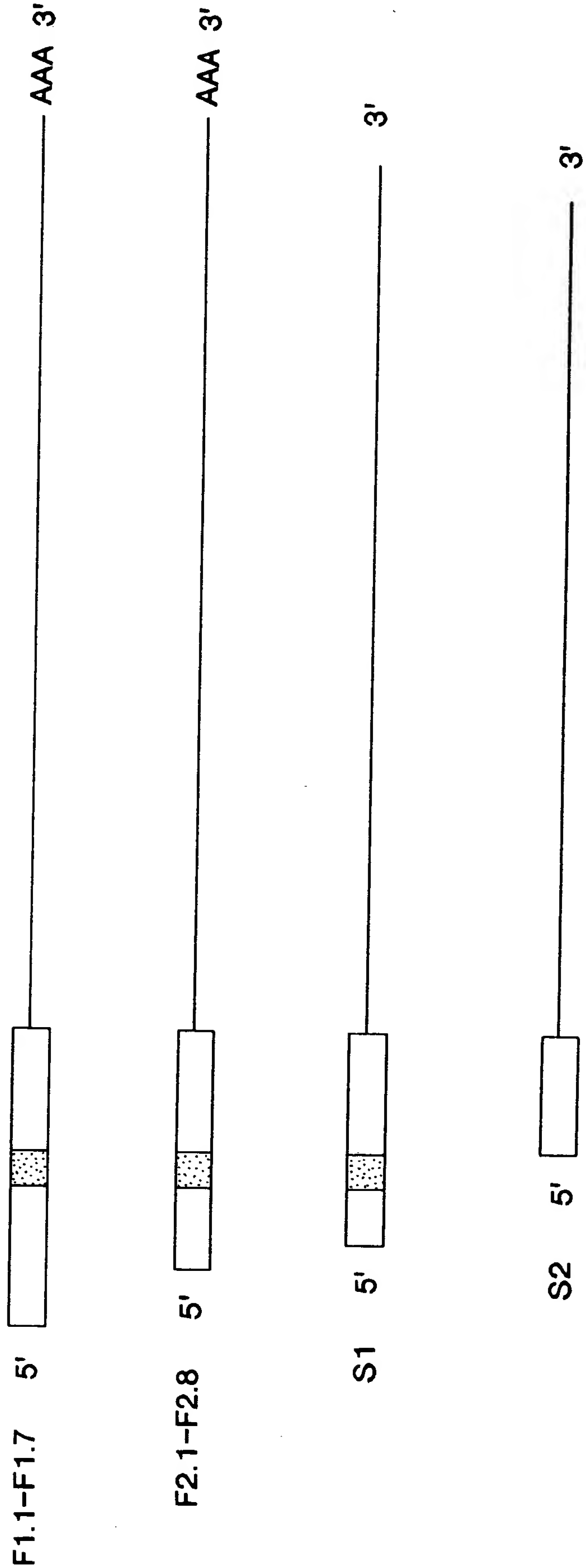


FIG. 5

```
  1 ACCCCCGAGAAAGCAACCCAGCGCGCCGCCCGCTCCTCACGTGTCCCTCCCGGCCCCGGG  60
 61 GCCACCTCACGTTCTGCTTCCGTCTGACCCCTCCGACTTCCGGTAAAGAGTCCCTATCCG 120
                            *
121 CACCTCCGCTCCCACCCGGCGCCTCGGCGCGCCCGCCCTCCGATGCGCTCAGCGGCCGCA 180
  1                                             M  R  S  A  A  A   6
181 GCTCCTCGGAGTCCCGCGGTGGCCACCGAGTCTCGCCGCTTCGCCGCAGCCAGGTGGCCC 240
  7 A  P  R  S  P  A  V  A  T  E  S  R  R  F  A  A  A  R  W  P    26
241 GGGTGGCGCTCGCTCCAGCGGCCGGCGCGGCGGAGCGGGCGGGGCGGCGGTGGCGCGGCC 300
 27 G  W  R  S  L  Q  R  P  A  R  R  S  G  R  G  G  G  G  A  A    46
301 CCGGGACCGTATCCCTCCGCCGCCCCTCCCCCGCCCGGCCCCGGCCCCCCTCCCTCCCGG 360
 47 P  G  P  Y  P  S  A  A  P  P  P  P  G  P  G  P  P  P  S  R    66
361 CAGAGCTCGCCTCCCTCCGCCTCAGACTGTTTTGGTAGCAACGGCAACGGCGGCGGCGCG 420
 67 Q  S  S  P  P  S  A  S  D  C  F  G  S  N  G  N  G  G  G  A    86
421 TTTCGGCCCGGCTCCCGGCGGCTCCTTGGTCTCGGCGGGCCTCCCCGCCCCTTCGTCGTC 480
 87 F  R  P  G  S  R  R  L  L  G  L  G  G  P  P  R  P  F  V  V   106
481 GTCCTTCTCCCCCTCGCCAGCCCGGGCGCCCCTCCGGCCGCGCCAACCCGCGCCTCCCCG 540
107 V  L  L  P  L  A  S  P  G  A  P  P  A  A  P  T  R  A  S  P   126
541 CTCGGCGCCCGTGCGTCCCCGCCGCGTTCCGGCGTCTCCTTGGCGCGCCCGGCTCCCGGC 600
127 L  G  A  R  A  S  P  P  R  S  G  V  S  L  A  R  P  A  P  G   146
                                         SCA2-A
601 TGTCCCCGCCCGGCGTGCGAGCCGGTGTATGGGCCCCTCACCATGTCGCTGAAGCCCCAG 660
147 C  P  R  P  A  C  E  P  V  Y  G  P  L  T  M  S  L  K  P  Q   166
661 CAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAG 720
167 Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q   186
```

FIG. 6A

```
                                   SCA2-B
721   CAGCCGCCGCCCGCGGCTGCCAATGTCCGCAAGCCCGGCGGCAGCGGCCTTCTAGCGTCG   780
187   Q  P  P  P  A  A  A  N  V  R  K  P  G  G  S  G  L  L  A  S    206
781   CCCGCCGCCGCGCCTTCGCCGTCCTCGTCCTCGGTCTCCTCGTCCTCGGCCACGGCTCCC   840
207   P  A  A  A  P  S  P  S  S  S  S  V  S  S  S  S  A  T  A  P    226
841   TCCTCGGTGGTCGCGGCGACCTCCGGCGGCGGGAGGCCCGGCCTGGGCAGAGGTCGAAAC   900
227   S  S  V  V  A  A  T  S  G  G  G  R  P  G  L  G  R  G  R  N    246
901   AGTAACAAAGGACTGCCTCAGTCTACGATTTCTTTTGATGGAATCTATGCAAATATGAGG   960
247   S  N  K  G  L  P  Q  S  T  I  S  F  D  G  I  Y  A  N  M  R    266
961   ATGGTTCATATACTTACATCAGTTGTTGGCTCCAAATGTGAAGTACAAGTGAAAAATGGA   1020
267   M  V  H  I  L  T  S  V  V  G  S  K  C  E  V  Q  V  K  N  G    286
                                                           SCA2-14B
1021  GGTATATATGAAGGAGTTTTTAAAACTTACAGTCCGAAGTGTGATTTGGTACTTGATGCC   1080
287   G  I  Y  E  G  V  F  K  T  Y  S  P  K  C  D  L  V  L  D  A    306
1081  GCACATGAGAAAAGTACAGAATCCAGTTCGGGGCCGAAACGTGAAGAAATAATGGAGAGT   1140
307   A  H  E  K  S  T  E  S  S  S  G  P  K  R  E  E  I  M  E  S    326
1141  ATTTTGTTCAAATGTTCAGACTTTGTTGTGGTACAGTTTAAAGATATGGACTCCAGTTAT   1200
327   I  L  F  K  C  S  D  F  V  V  V  Q  F  K  D  M  D  S  S  Y    346
1201  GCAAAAAGAGATGCTTTTACTGACTCTGCTATCAGTGCTAAAGTGAATGGCGAACACAAA   1260
347   A  K  R  D  A  F  T  D  S  A  I  S  A  K  V  N  G  E  H  K    366
1261  GAGAAGGACCTGGAGCCCTGGGATGCAGGTGAACTCACAGCCAATGAGGAACTTGAGGCT   1320
367   E  K  D  L  E  P  W  D  A  G  E  L  T  A  N  E  E  L  E  A    386
1321  TTGGAAAATGACGTATCTAATGGATGGGATCCCAATGATATGTTTCGATATAATGAAGAA   1380
387   L  E  N  D  V  S  N  G  W  D  P  N  D  M  F  R  Y  N  E  E    406
1381  AATTATGGTGTAGTGTCTACGTATGATAGCAGTTTATCTTCGTATACAGTGCCCTTAGAA   1440
407   N  Y  G  V  V  S  T  Y  D  S  S  L  S  S  Y  T  V  P  L  E    426
1441  AGAGATAACTCAGAAGAATTTTTAAAACGGGAAGCAAGGGCAAACCAGTTAGCAGAAGAA   1500
427   R  D  N  S  E  E  F  L  K  R  E  A  R  A  N  Q  L  A  E  E    446
```

FIG. 6B

```
1501  ATTGAGTCAAGTGCCCAGTACAAAGCTCGAGTGGCCCTGGAAAATGATGATAGGAGTGAG  1560
447   I  E  S  S  A  Q  Y  K  A  R  V  A  L  E  N  D  D  R  S  E   466
1561  GAAGAAAAATACACAGCAGTTCAGAGAAATTCCAGTGAACGTGAGGGGCACAGCATAAAC  1620
467   E  E  K  Y  T  A  V  Q  R  N  S  S  E  R  E  G  H  S  I  N   486
1621  ACTAGGGAAAATAAATATATTCCTCCTGGACAAAGAAATAGAGAAGTCATATCCTGGGGA  1680
487   T  R  E  N  K  Y  I  P  P  G  Q  R  N  R  E  V  I  S  W  G   506
1681  AGTGGGAGACAGAATTCACCGCGTATGGGCCAGCCTGGATCGGGCTCCATGCCATCAAGA  1740
507   S  G  R  Q  N  S  P  R  M  G  Q  P  G  S  G  S  M  P  S  R   526
1741  TCCACTTCTCACACTTCAGATTTCAACCCGAATTCTGGTTCAGACCAAAGAGTAGTTAAT  1800
527   S  T  S  H  T  S  D  F  N  P  N  S  G  S  D  Q  R  V  V  N   546
1801  GGAGGTGTTCCCTGGCCATCGCCTTGCCCATCTCCTTCCTCTCGCCCACCTTCTCGCTAC  1860
547   G  G  V  P  W  P  S  P  C  P  S  P  S  S  R  P  P  S  R  Y   566
1861  CAGTCAGGTCCCAACTCTCTTCCACCTCGGGCAGCCACCCCTACACGGCCGCCCTCCAGG  1920
567   Q  S  G  P  N  S  L  P  P  R  A  A  T  P  T  R  P  P  S  R   586
1921  CCCCCCTCGCGGCCATCCAGACCCCCGTCTCACCCCTCTGCTCATGGTTCTCCAGCTCCT  1980
587   P  P  S  R  P  S  R  P  P  S  H  P  S  A  H  G  S  P  A  P   606
1981  GTCTCTACTATGCCTAAACGCATGTCTTCAGAAGGGCCTCCAAGGATGTCCCCAAAGGCC  2040
607   V  S  T  M  P  K  R  M  S  S  E  G  P  P  R  M  S  P  K  A   626
2041  CAGCGACATCCTCGAAATCACAGAGTTTCTGCTGGGAGGGGTTCCATATCCAGTGGCCTA  2100
627   Q  R  H  P  R  N  H  R  V  S  A  G  R  G  S  I  S  S  G  L   646
2101  GAATTTGTATCCCACAACCCACCCAGTGAAGCAGCTACTCCTCCAGTAGCAAGGACCAGT  2160
647   E  F  V  S  H  N  P  P  S  E  A  A  T  P  P  V  A  R  T  S   666
2161  CCCTCGGGGGGAACGTGGTCATCAGTGGTCAGTGGGGTTCCAAGATTATCCCCTAAAACT  2220
667   P  S  G  G  T  W  S  S  V  V  S  G  V  P  R  L  S  P  K  T   686
2221  CATAGACCCAGGTCTCCCAGACAGAACAGTATTGGAAATACCCCCAGTGGGCCAGTTCTT  2280
687   H  R  P  R  S  P  R  Q  N  S  I  G  N  T  P  S  G  P  V  L   706
```

FIG. 6C

```
2281 GCTTCTCCCCAAGCTGGTATTATTCCAACTGAAGCTGTTGCCATGCCTATTCCAGCTGCA 2340
 707  A  S  P  Q  A  G  I  I  P  T  E  A  V  A  M  P  I  P  A  A   726
2341 TCTCCTACGCCTGCTAGTCCTGCATCGAACAGAGCTGTTACCCCTTCTAGTGAGGCTAAA 2400
 727  S  P  T  P  A  S  P  A  S  N  R  A  V  T  P  S  S  E  A  K   746
2401 GATTCCAGGCTTCAAGATCAGAGGCAGAACTCTCCTGCAGGGAATAAAGAAAATATTAAA 2460
 747  D  S  R  L  Q  D  Q  R  Q  N  S  P  A  G  N  K  E  N  I  K   766
2461 CCCAATGAAACATCACCTAGCTTCTCAAAAGCTGAAAACAAAGGTATATCACCAGTTGTT 2520
 767  P  N  E  T  S  P  S  F  S  K  A  E  N  K  G  I  S  P  V  V   786
2521 TCTGAACATAGAAAACAGATTGATGATTTAAAGAAATTTAAGAATGATTTTAGGTTACAG 2580
 787  S  E  H  R  K  Q  I  D  D  L  K  K  F  K  N  D  F  R  L  Q   806
2581 CCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAGGGAGAAAAA 2640
 807  P  S  S  T  S  E  S  M  D  Q  L  L  N  K  N  R  E  G  E  K   826
2641 TCAAGAGATTTGATCAAAGACAAAATTGAACCAAGTGCTAAGGATTCTTTCATTGAAAAT 2700
 827  S  R  D  L  I  K  D  K  I  E  P  S  A  K  D  S  F  I  E  N   846
2701 AGCAGCAGCAACTGTACCAGTGGCAGCAGCAAGCCGAATAGCCCCAGCATTTCCCCTTCA 2760
 847  S  S  S  N  C  T  S  G  S  S  K  P  N  S  P  S  I  S  P  S   866
2761 ATACTTAGTAACACGGAGCACAAGAGGGGACCTGAGGTCACTTCCCAAGGGGTTCAGACT 2820
 867  I  L  S  N  T  E  H  K  R  G  P  E  V  T  S  Q  G  V  Q  T   886
2821 TCCAGCCCAGCATGTAAACAAGAGAAAGACGATAAGGAAGAGAAGAAAGACGCAGCTGAG 2880
 887  S  S  P  A  C  K  Q  E  K  D  D  K  E  E  K  K  D  A  A  E   906
2881 CAAGTTAGGAAATCAACATTGAATCCCAATGCAAAGGAGTTCAACCCACGTTCCTTCTCT 2940
 907  Q  V  R  K  S  T  L  N  P  N  A  K  E  F  N  P  R  S  F  S   926
2941 CAGCCAAAGCCTTCTACTACCCCAACTTCACCTCGGCCTCAAGCACAACCTAGCCCATCT 3000
 927  Q  P  K  P  S  T  T  P  T  S  P  R  P  Q  A  Q  P  S  P  S   946
3001 ATGGTGGGTCATCAACAGCCAACTCCAGTTTATACTCAGCCTGTTTGTTTTGCACCAAAT 3060
 947  M  V  G  H  Q  Q  P  T  P  V  Y  T  Q  P  V  C  F  A  P  N   966
3061 ATGATGTATCCAGTCCCAGTGAGCCCAGGCGTGCAACCTTTATACCCAATACCTATGACG 3120
 967  M  M  Y  P  V  P  V  S  P  G  V  Q  P  L  Y  P  I  P  M  T   986
```

FIG. 6D

```
3121  CCCATGCCAGTGAATCAAGCCAAGACATATAGAGCAGTACCAAATATGCCCCAACAGCGG  3180
 987  P  M  P  V  N  Q  A  K  T  Y  R  A  V  P  N  M  P  Q  Q  R  1006
3181  CAAGACCAGCATCATCAGAGTGCCATGATGCACCCAGCGTCAGCAGCGGGCCCACCGATT  3240
1007  Q  D  Q  H  H  Q  S  A  M  M  H  P  A  S  A  A  G  P  P  I  1026
3241  GCAGCCACCCCACCAGCTTACTCCACGCAATATGTTGCCTACAGTCCTCAGCAGTTCCCA  3300
1027  A  A  T  P  P  A  Y  S  T  Q  Y  V  A  Y  S  P  Q  Q  F  P  1046
3301  AATCAGCCCCTTGTTCAGCATGTGCCACATTATCAGTCTCAGCATCCTCATGTCTATAGT  3360
1047  N  Q  P  L  V  Q  H  V  P  H  Y  Q  S  Q  H  P  H  V  Y  S  1066
3361  CCTGTAATACAGGGTAATGCTAGAATGATGGCACCACCAACACACGCCCAGCCTGGTTTA  3420
1067  P  V  I  Q  G  N  A  R  M  M  A  P  P  T  H  A  Q  P  G  L  1086
3421  GTATCTTCTTCAGCAACTCAGTACGGGGCTCATGAGCAGACGCATGCGATGTATGCATGT  3480
1087  V  S  S  S  A  T  Q  Y  G  A  H  E  Q  T  H  A  M  Y  A  C  1106
3481  CCCAAATTACCATACAACAAGGAGACAAGCCCTTCTTTCTACTTTGCCATTTCCACGGGC  3540
1107  P  K  L  P  Y  N  K  E  T  S  P  S  F  Y  F  A  I  S  T  G  1126
3541  TCCCTTGCTCAGCAGTATGCGCACCCTAACGCTACCCTGCACCCACATACTCCACACCCT  3600
1127  S  L  A  Q  Q  Y  A  H  P  N  A  T  L  H  P  H  T  P  H  P  1146
3601  CAGCCTTCAGCTACCCCCACTGGACAGCAGCAAAGCCAACATGGTGGAAGTCATCCTGCA  3660
1147  Q  P  S  A  T  P  T  G  Q  Q  Q  S  Q  H  G  G  S  H  P  A  1166
3661  CCCAGTCCTGTTCAGCACCATCAGCACCAGGCCGCCCAGGCTCTCCATCTGGCCAGTCCA  3720
```

FIG. 6E

```
1167  P  S  P  V  Q  H  H  Q  H  Q  A  A  Q  A  L  H  L  A  S  P   1186
3721  CAGCAGCAGTCAGCCATTTACCACGCGGGCTTGCGCCAACTCCACCCTCCATGACACCT   3780
1187  Q  Q  Q  S  A  I  Y  H  A  G  L  A  P  T  P  P  S  M  T  P   1206
3781  GCCTCCAACACGCAGTCGCCACAGAATAGTTTCCCAGCAGCACAACAGACTGTCTTTACG   3840
1207  A  S  N  T  Q  S  P  Q  N  S  F  P  A  A  Q  Q  T  V  F  T   1226
3841  ATCCATCCTTCTCACGTTCAGCCGGCGTATACCAACCCACCCCACATGGCCCACGTACCT   3900
1227  I  H  P  S  H  V  Q  P  A  Y  T  N  P  P  H  M  A  H  V  P   1246
3901  CAGGCTCATGTACAGTCAGGAATGGTTCCTTCTCATCCAACTGCCCATGCGCCAATGATG   3960
1247  Q  A  H  V  Q  S  G  M  V  P  S  H  P  T  A  H  A  P  M  M   1266
3961  CTAATGACGACACAGCCACCCGGCGGTCCCCAGGCCGCCCTCGCTCAAAGTGCACTACAG   4020
1267  L  M  T  T  Q  P  P  G  G  P  Q  A  A  L  A  Q  S  A  L  Q   1286
4021  CCCATTCCAGTCTCGACAACAGCGCATTTCCCCTATATGACGCACCCTTCAGTACAAGCC   4080
1287  P  I  P  V  S  T  T  A  H  F  P  Y  M  T  H  P  S  V  Q  A   1306
4081  CACCACCAACAGCAGTTGTAAGGCTGCCCTGGAGGAACCGAAAGGCCAAATTCCCTCCTC   4140
1307  H  H  Q  Q  Q  L  *                                            1326
4141  CCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAACTAGAATTTCATTTATTTTGTTTT   4200
4201  TAAAATATATATGTTGATTTCTTGTAACATCCAATAGGAATGCTAACAGTTCACTTGCAG   4260
4261  TGGAAGATACTTGGACCGAGTAGAGGCATTTAGGAACTTGGGGGCTATTCCATAATTCCA   4320
4321  TATGCTGTTTCAGAGTCCCGCAGGTACCCCAGCTCTGCTTGCCGAAACTGGAAGTTATTT   4380
4381  ATTTTTTAATAACCCTTGAAAGTCATGAACACATCAGCTAGCAAAAGAAGTAACAAGAGT   4440
4441  GATTCTTGCTGCTATTACTGCTAAAAAAAAAAAAAAAAAAA   4481
```

FIG. 6F

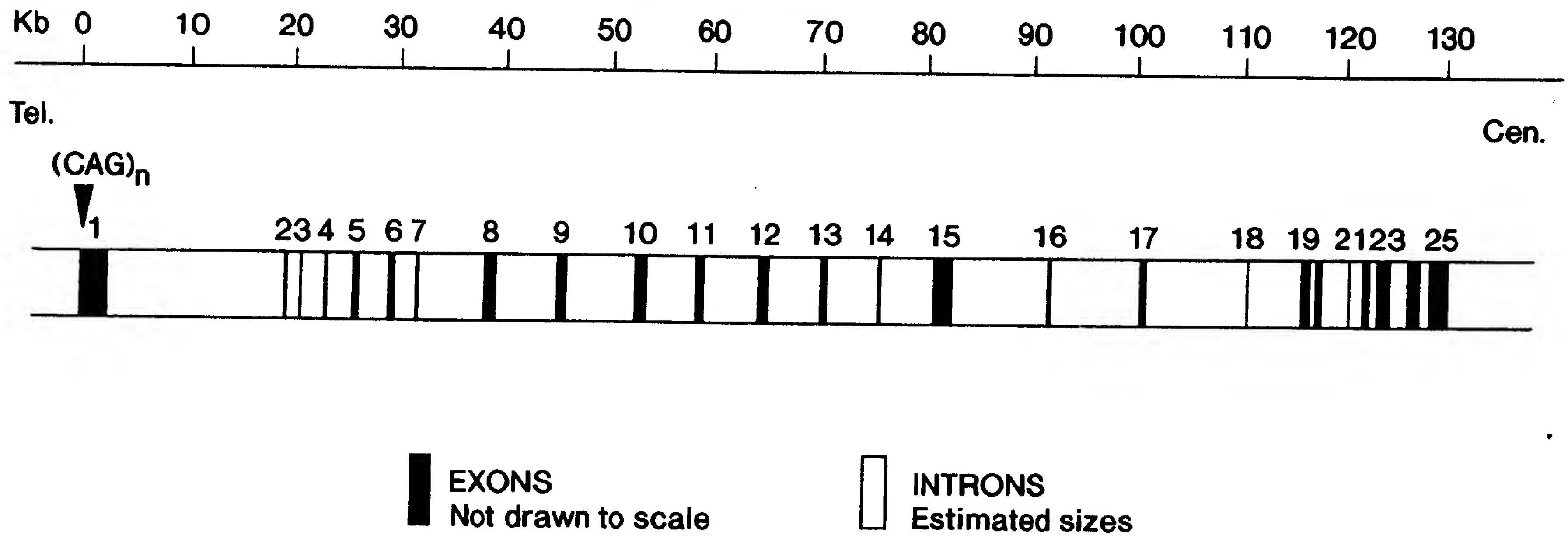
```
                  1                                                      50
Ataxin-2          VYGPLTMSLK PQQQQQQQQQ QQQQQQQQQQ QQQPPPAAAN VRKPGGSGLL
Mouse Ataxin-2    HEGPLTMSLK PQPQ...... .......... ....PPAPAT GRKPGG.GLL
A2RP              ........LA PQPPPPQQHQ ER........ .......... ..........
       Consensus  --------L- PQ-------- ---------- ---------- ----------

                  51                                                    100
Ataxin-2          ASPAAAPSPS SSSVSSSSAT APSSVVA... ATSGGGRPGL GRGRNSNKGL
Mouse Ataxin-2     SSPGAAP.AS AAVTSASVVP APAAPVASSS AAAGGGRPGL GRGRNSSKGL
A2RP              ..PGAAAIGS A......... .......... .......... .RGQSTGKGP
       Consensus  --P-AA---S ---------- ---------- ---------- -RG----KG-

                  101                                                   150
Ataxin-2          PQSTISFDGI YANMRMVHIL TSVVGSKCEV QVKNGGIYEG VFKTYSPKCD
Mouse Ataxin-2    PQPTISFDGI YANVRMVHIL TSVVGSKCEV QVKNGGIYEG VFKTYSPKCD
A2RP              PQSPV.FEGV YNNSRMLHFL TAVVGSTCDV KVKNGTTYEG IFKTLSSKFE
       Consensus  PQ----F-G- Y-N-RM-H-L T-VVGS-C-V -VKNG--YEG -FKT-S-K--

                  151                                                   200
Ataxin-2          LVLDAAHEKS TESSSGPKRE EIMESILFKC SDFVVVQFKD MDSSYAKRDA
Mouse Ataxin-2    LVLDAAHEKS TESSSGPKRE EIMESVLFKC SDFVVVQFKD TDSSYARRDA
A2RP              LAVDAVHRKA SEPAGGPRRE DIVDTMVFKP SDVMLVHFRN VDFNYATKDK
       Consensus  L--DA-H-K- -E---GP-RE -I-----FK- SD---V-F-- -D--YA--D-
```

FIG. 7A

```
                 201                                                  250
Ataxin-2         FTDSAIS..A KVNGEHKEKD LEPWDAGELT ANEELEALEN DVSNGWDPND
Mouse Ataxin-2   FTDSALS..A KVNGEHKEKD LEPWDAGELT ASEELE.LEN DVSNGWDPND
A2RP             FTDSAIAMNS KVNGEHKEKV LQRWEGGD.S NSDDYD.LES DMSNGWDPNE
       Consensus FTDSA----- KVNGEHKEK- L--W--G--- -------LE- D-SNGWDPN-

                 251                                                  300
Ataxin-2         MFRYNEENYG VVSTYDSSLS SYTVPLERDN SEEFLKREAR ANQLAEEIES
Mouse Ataxin-2   MFRYNEENYG VVSTYDSSLS SYTVPLERDN SEEFLKREAR ANQLAEEIES
A2RP             MFKFNEENYG VKTTYDSSLS SYTVPLEKDN SEEFRQRELR AAQLAREIES
       Consensus MF--NEENYG V--TYDSSLS SYTVPLE-DN SEEF--RE-R A-QLA-EIES

                 301                                                  350
Ataxin-2         SAQYKARVAL ENDD.RSEEE KYTAVQRNSS EREGHSINTR ENKYIPPGQR
Mouse Ataxin-2   SAQYKARVAL ENDD.RSEEE KYTAVQRNCS DREGHGPNTR DNKYIPPGQR
A2RP             SPQYRLRIAM ENDDGRTEEE KHSAVQRQGS GRESPSLASR EGKYIP....
       Consensus S-QY--R-A- ENDD-R-EEE K--AVQR--S -RE------R --KYIP----

                 351
Ataxin-2         NR
Mouse Ataxin-2   NR
A2RP             ..
       Consensus --
```

FIG. 7B

SCA2 Gene



-Largest exon: exon 1, 928 bps; contains CAG repeat
-Largest intron: intron 1 with approximately 15 Kbps
-Smallest exon: exon 2, 37 bps

- Exon sizes:
  8<100 bps
  100 bps<12<200 bps
  200 bps< 4<400 bps
  400 bps< 1

- known intron sizes:
  intron 2 : 1.6 Kb
  intron 19: 0.3 Kb
  intron 22: 1.0 Kb
  intron 24: 1.6 Kb

FIG. 8